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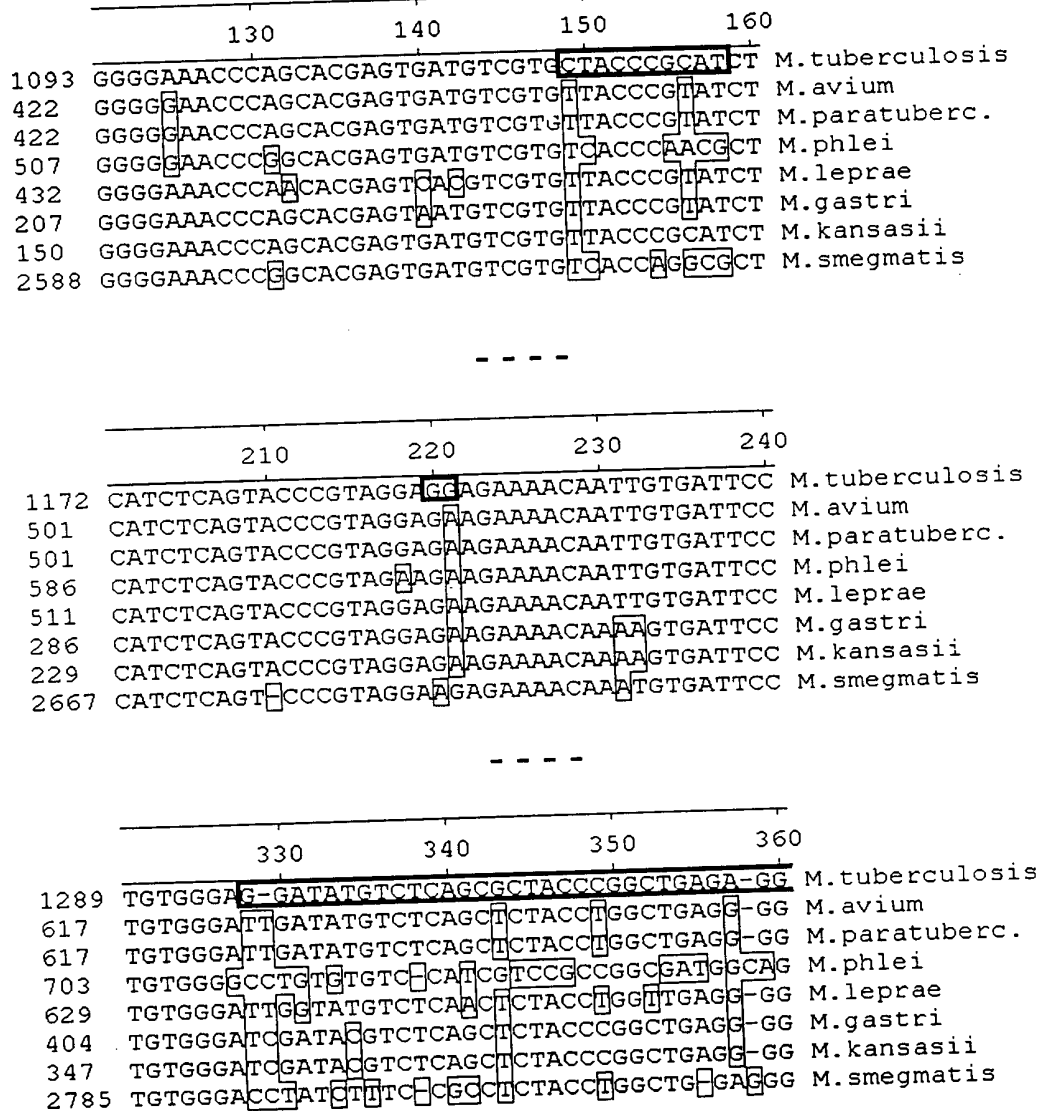


Figure 1A

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	370	380	390	400	
1327	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.tuberculosis
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.avium
656	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.paratuberc.
742	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.phlei
668	TAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.leprae
443	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.gastri
386	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.kansasii
2823	CAGTCAGAAAGTGTCTGGTTAGCGGAAGTGGCCTGGGAT				M.smegmatis

	450	460	470	480	
1406	CGGCACCTGCCTTATCAATTCCCGAGTAGCAGCGGGCC				M.tuberculosis
735	CGGCACCTGCCTTATCAATACCCGAGTAGCAGCGGGCC				M.avium
735	CGGCACCTGCCTTATCAATACCCGAGTAGCAGCGGGCC				M.paratuberc.
820	TGCTGCCGCTGTACAGG--TCCCGAGTAGCAGCGGGCC				M.phlei
747	TGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M.leprae
522	CGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M.gastri
465	CGGCACCTGCCTTGTATCAATTCCCGAGTAGCAGCGGGCC				M.kansasii
2902	CGACGTCTGTCTTGTATGGTGTCCCGAGTAGCAGCGGGCC				M.smegmatis

	490	500	510	520	
1446	CGTGGAATCGCTGTGAATCCGCCGGGACCACCCGGTAAG				M.tuberculosis
775	CGTGGAATCGCTGTGAATCGGCCGGGACCACCCGGTAAG				M.avium
775	CGTGGAATCGCTGTGAATCGGCCGGGACCACCCGGTAAG				M.paratuberc.
857	CGTGGAATCGCTGTGAATCGGCCGGGACCACCCGGTAAG				M.phlei
787	CGTGGAATCGCTGTGAATCGGCCGGGACCACCCGGTAAG				M.leprae
562	CGTGGAATCGCTGTGAATCGGCCGGGACCACCCGGTAAG				M.gastri
505	CGTGGAATCGCTGTGAATCGGCCGGGACCACCCGGTAAG				M.kansasii
2942	CGTGGAATCGCTGTGAATCGGCCGGGACCACCCGGTAAG				M.smegmatis

Figure 1B

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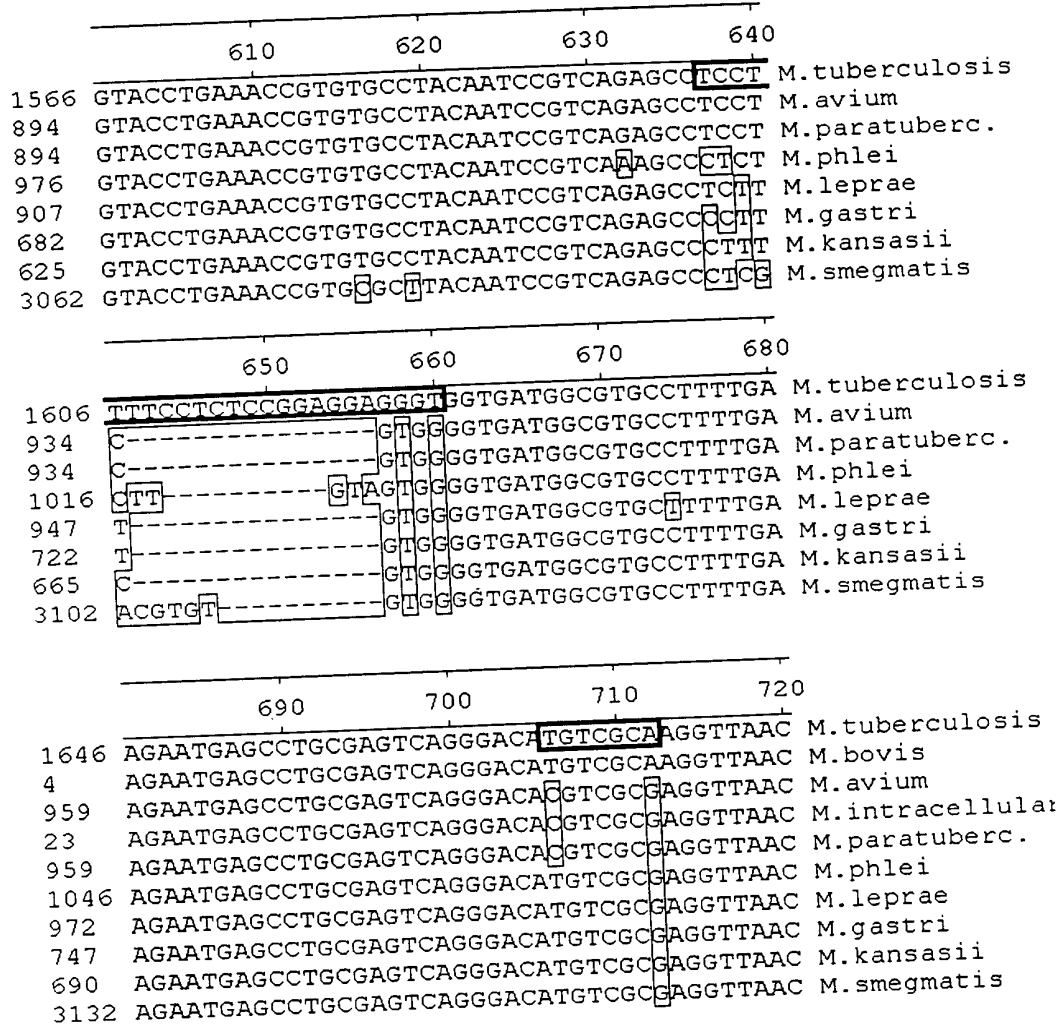


Figure 1C

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		770	780	790	800	
1726	CGACCCACACGCGCATACGCGCGTGTGAA					M.tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT					M.bovis
1039	CG-----CATCCCTTTTGGGGTGT					M.avium
103	CG-----CATCCCTTTTGGGGTGT					M.intracellula
1039	CG-----CATCCCTTTTGGGGTGT					M.paratuberc.
1126	CGTATCAACCTGTTGGGGTTGGTGT					M.phlei
1052	CGTAT--CACGTTGTGAGCGTGTGT					M.leprae
827	CGTAT--CACGCGTAAGCGTGTGT					M.gastri
770	CGTAT--CGCGCGSAGCGTGTGT					M.kansasii
3212	CGTAT--CCACACAAGAGTGTGTGGTGT					M.smegmatis

		970	980	990	1000	
1926	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG					M.tuberculosis
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG					M.avium
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG					M.paratuberc.
1322	ATTTAGGTGCAGCGTGGCTGTTTATCGGAGGTAGAG					M.phlei
1244	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG					M.leprae
1019	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG					M.gastri
962	ATTTAGGTGCAGCGTTGCGTGGTTCACCGCGGAGGTAGAG					M.kansasii
3408	ATTTAGGTGCAGCGTGGCTGTTTTCGCGGAGGTAGAG					M.smegmatis

		1050	1060	1070	1080	
2005	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AAGCGTGGCA					M.tuberculosis
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AAGCGTGGCA					M.avium
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AAGCGTGGCA					M.paratuberc.
1401	CAGCCAAACTCCGAATGCCG-TAAG-TA-AAGTGGCA					M.phlei
1323	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AAGCGTGGCA					M.leprae
1098	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AAGCGTGGCA					M.gastri
1041	CAGCCAAACTCCGAATGCCG-TGGTG-TA-AAGCGTGGCA					M.kansasii
3486	CAGCCAAACTCCGAATGCCG-TAAGGCAAGAGTGGCA					M.smegmatis

Figure 1D

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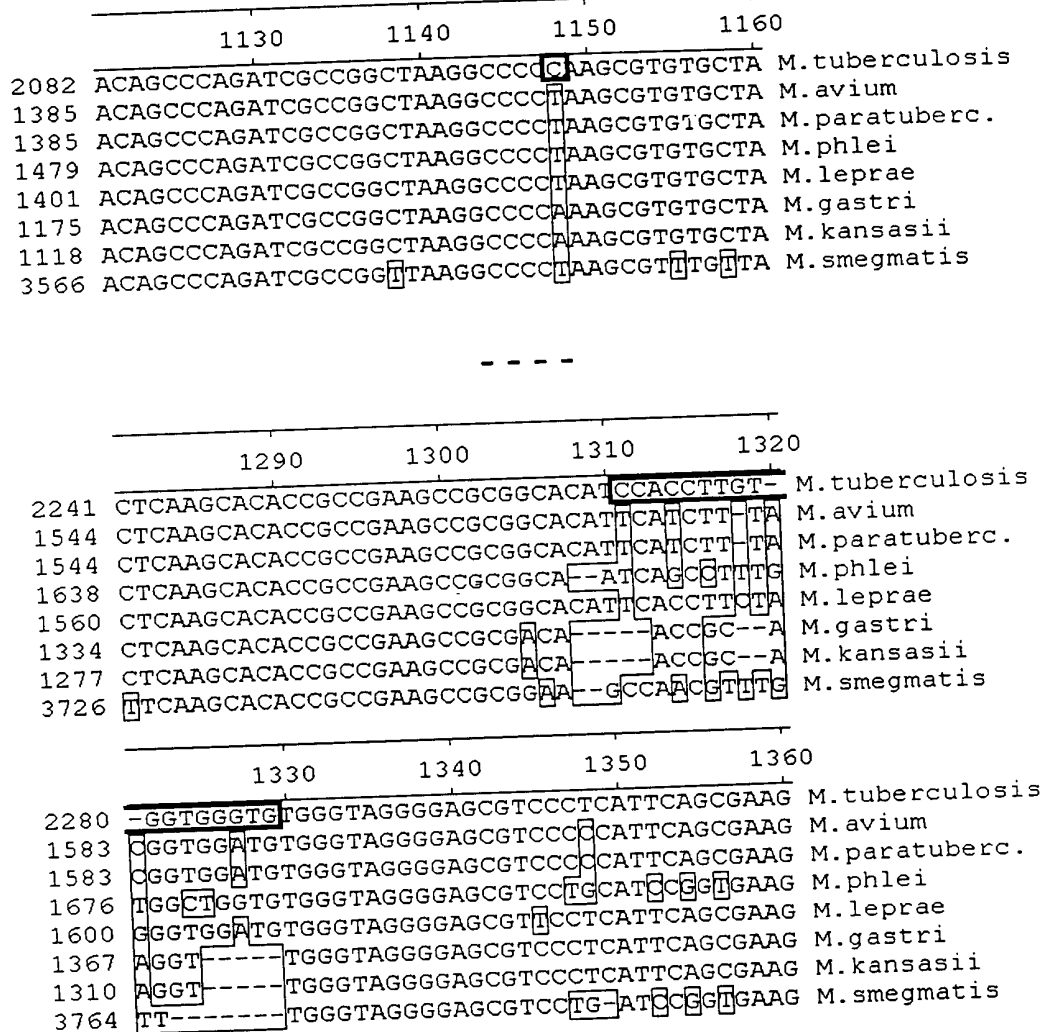


Figure 1E

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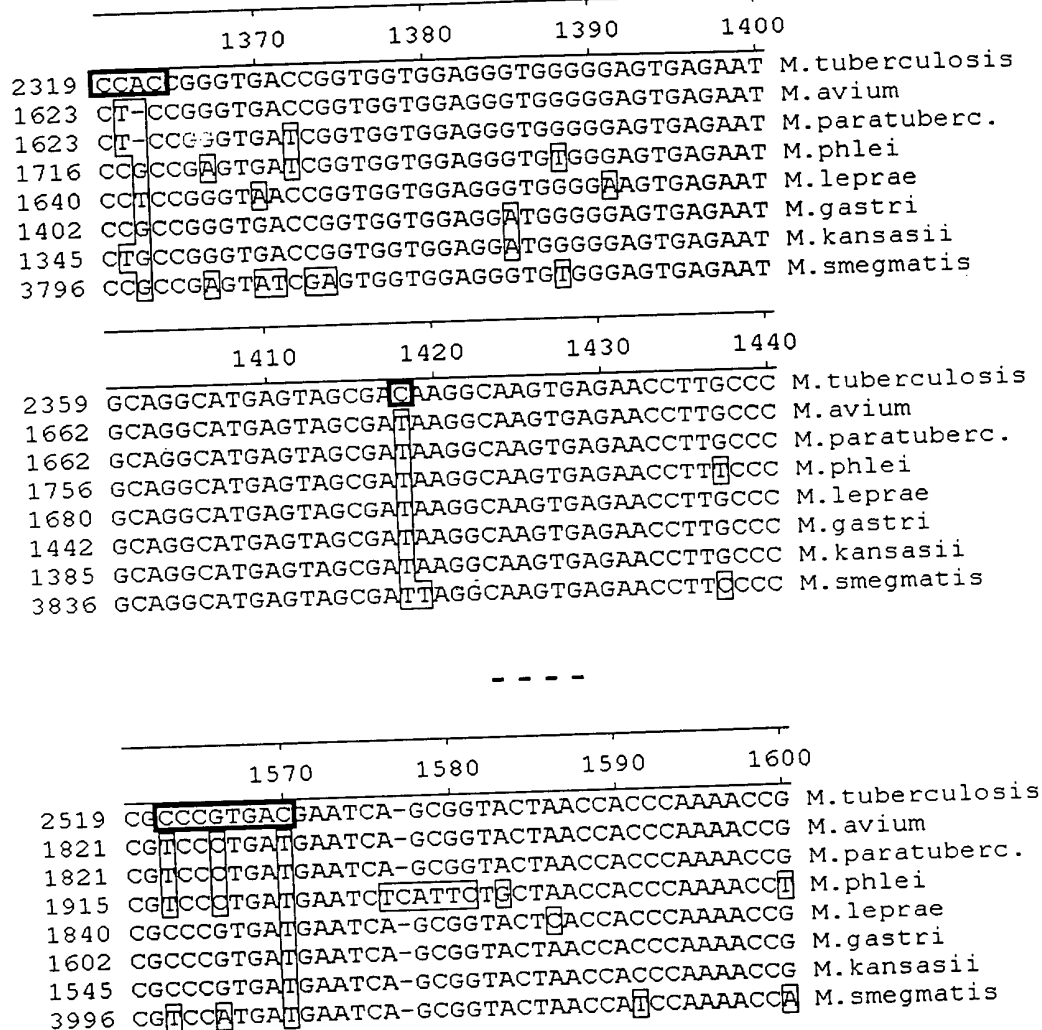


Figure 1F

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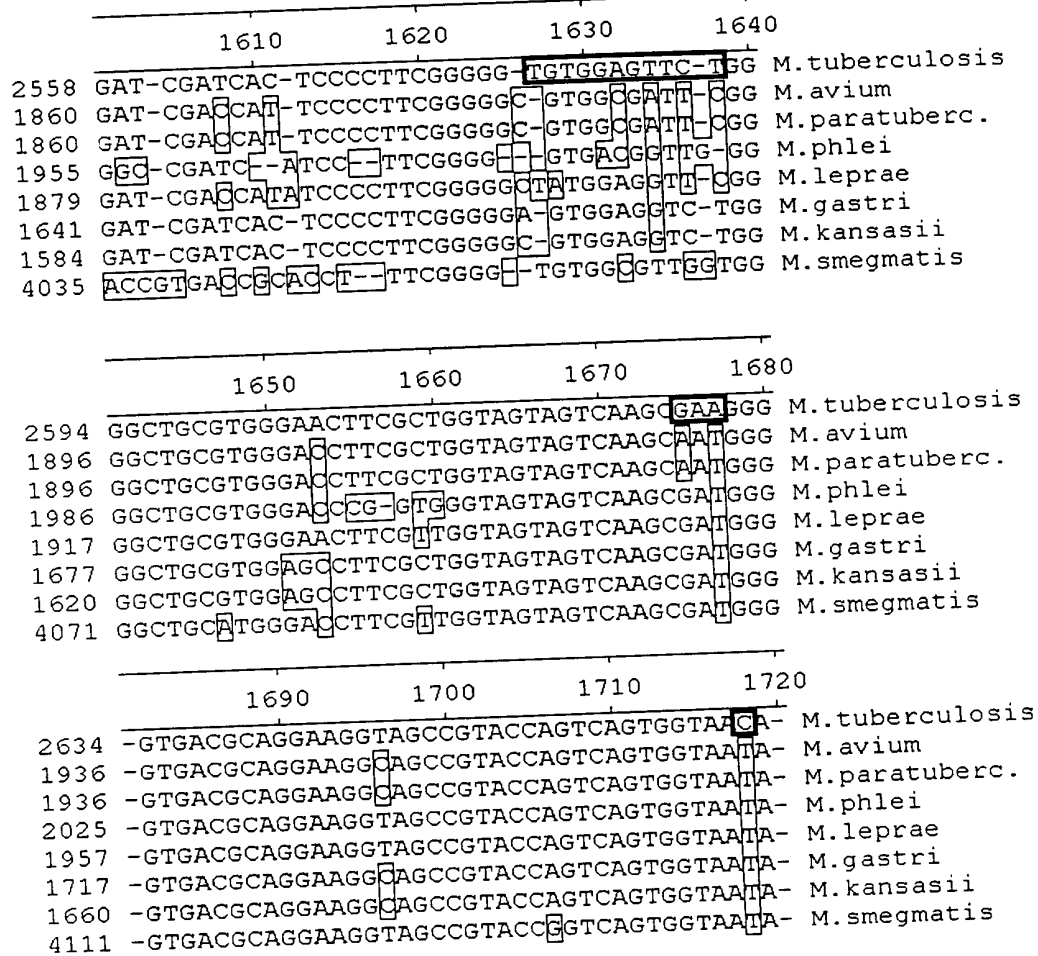


Figure 1G

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1730 1740 1750 1760

2672 -CTGGGGCAAGCCGGTAGGGAGAGCGATAGGCAAATCCGT M.tuberculosis
 1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.avium
 1974 -CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAAATCCGT M.paratuberc.
 2063 -CTGGGGTAAACCTGTAGGGGAGAGGATAGGCAAATCCGT M.phlei
 1995 -CTGGAGCAAGCCCGTAGGGAGAGCGATAGGCAAATCCGT M.leprae
 1755 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.gastri
 1698 -CTGGGGCAAGCCAGTAGGGAGAGCGATAGGCAAATCCGT M.kansasii
 4149 -CTGGGGTAAAGCCGTGTAGGGAGTCAGATAGGTTAAATCCGT M.smegmatis

1970 1980 1990 2000

2908 AGGGGGACCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.tuberculosis
 2208 AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.avium
 2208 AGGGGGCCCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.paratuberc.
 2298 AGGGGGACCCACGTACCGTGAGGGCTCTTGCGGGGGAGC M.phlei
 2231 AGGGGGCCCGGAATATCGTGAACACCCTTGCGGTGGGAGC M.leprae
 1910 M.gastri
 1934 AGGGGGACCGGAATACCGTGAACACCCTTGCGGTGGGAGC M.kansasii
 4385 AGGGGGACCCACATGGCGTGTAAGCCCTTACGGCCCAAGC M.smegmatis

2410 2420 2430 2440

3345 ACCTCGACGCCAGTTGGGGCGGAGTCGTTGTTGAAATACC M.tuberculosis
 284 ACCTCGACGCCAGTTGGGGCGGAGTCGTTGTTGAAATACC M.bovis
 2645 GCACAGACGCCAGTTGGTGGAGTCGTTGTTGAAATACC M.avium
 393 ATACAGACGCCAGTTGTATGGAGTCGTTGTTGAAATACC M.intracellulare
 2645 GCACAGACGCCAGTTGGTGGAGTCGTTGTTGAAATACC M.paratuberc.
 2737 GCTCGGACGCCAGTTGGGTGGAGTCGTTGTTGAAATACC M.phlei
 2668 ACCTCGACGCCAGTTGGGTGGAGTCGTTGTTGAAATACC M.leprae
 1910 M.gastri
 2372 ACCTCAACGCCAGTTGGGGTGGAGTCGTTGTTGAAATACC M.kansasii
 4822 GCTCACAGGCCAGTTGGGTGGAGTCGTTGTTGAAATACC M.smegmatis

Figure 1H

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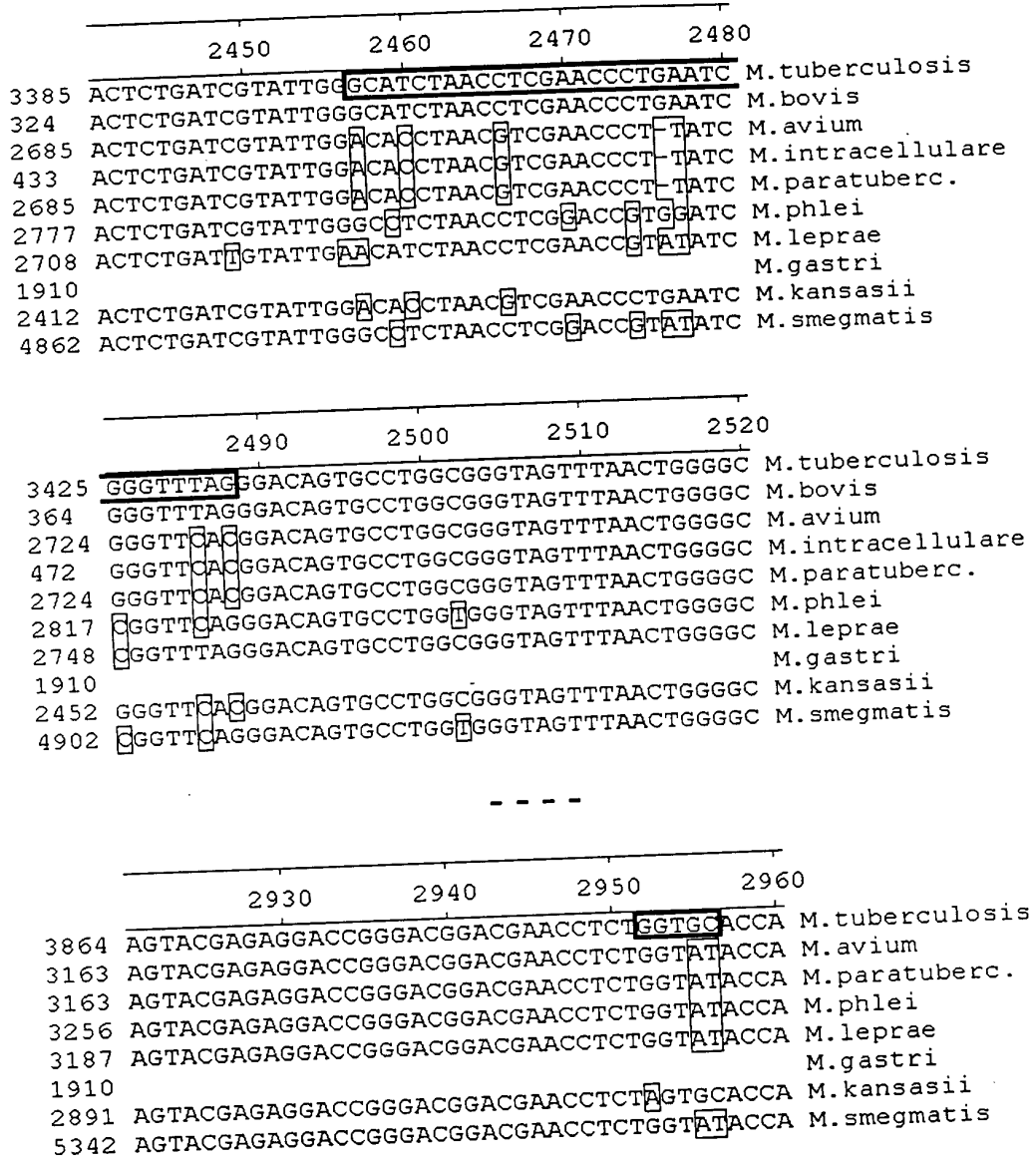


Figure 11

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	2970	2980	2990	3000	
3904	GTTGT	CCCC	CCAGGGGCACCGCTGGATAGCCACGTT	CGGT	M.tuberculosis
3203	GTTGT	CCCC	CCAGGGGCACCGCTGGATAGCCACGTT	CGGA	M.avium
3203	GTTGT	CCCC	CCAGGGGCACCGCTGGATAGCCACGTT	CGGA	M.paratuberc.
3296	GTTGT	CCCC	CCAGGGGCACCGCTGGATAGCCACGTT	CGGA	M.phlei
3227	GTTGT	CT	CCAGGGGCACCGCTGGATAGCCACGTT	CGGA	M.leprae
1910					M.gastri
2931	GTTGT	CCCC	CCAGGGGCACCGCTGGATAGC	ACGTT	M.kansasii
5382	GTTGT	CCCC	CCAGGGGCACCGCTGGATAGCCACGTT	CGGA	M.smegmatis

	3010	3020	3030	3040	
3944	CAG	GATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC			M.tuberculosis
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.avium
3243	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.paratuberc.
3336	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCT	CTTC			M.phlei
3267	CAG	GATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC			M.leprae
1910					M.gastri
2971	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCTTCTC				M.kansasii
5422	CAGGATAACCGCTGAAAGCATCTAAGCGGGAAACCT	CTTC			M.smegmatis

- - - -

	3090	3100	3110	3120	
4023	CCCGC-AGAACACGGG	TTCAATAGGT	CAGACCTGGAAGCT		M.tuberculosis
609	CCCGC-AGAACACGGG	TTCAATAGGT	CAGACCTGGAAGCT		M.bovis
3322	CCCGC-AGA	CACGGGATTGATAGG	CAGACCTGGAAGCT		M.avium
677	CCCGC-AGA	CACGGGTTGATAGG	CAGACCTGGAAGCT		M.intracellulare
3322	CCCGC-AGA	TACGGGATTGATAGG	CAGACCTGGAAGCT		M.paratuberc.
3415	CCCGC-AGA	CACGGGATCGATAG	ACAGACCTG	ACGCA	M.phlei
3309					M.leprae
1910					M.gastri
3050	CCCGC-AGA	CACGGGTTGATAGG	CAGACCTGGAAGCT		M.kansasii
5501	CCCGC-AGA	CACGGGATTGATAG	ACAGACCTGGAAGC		M.smegmatis

Figure 1J

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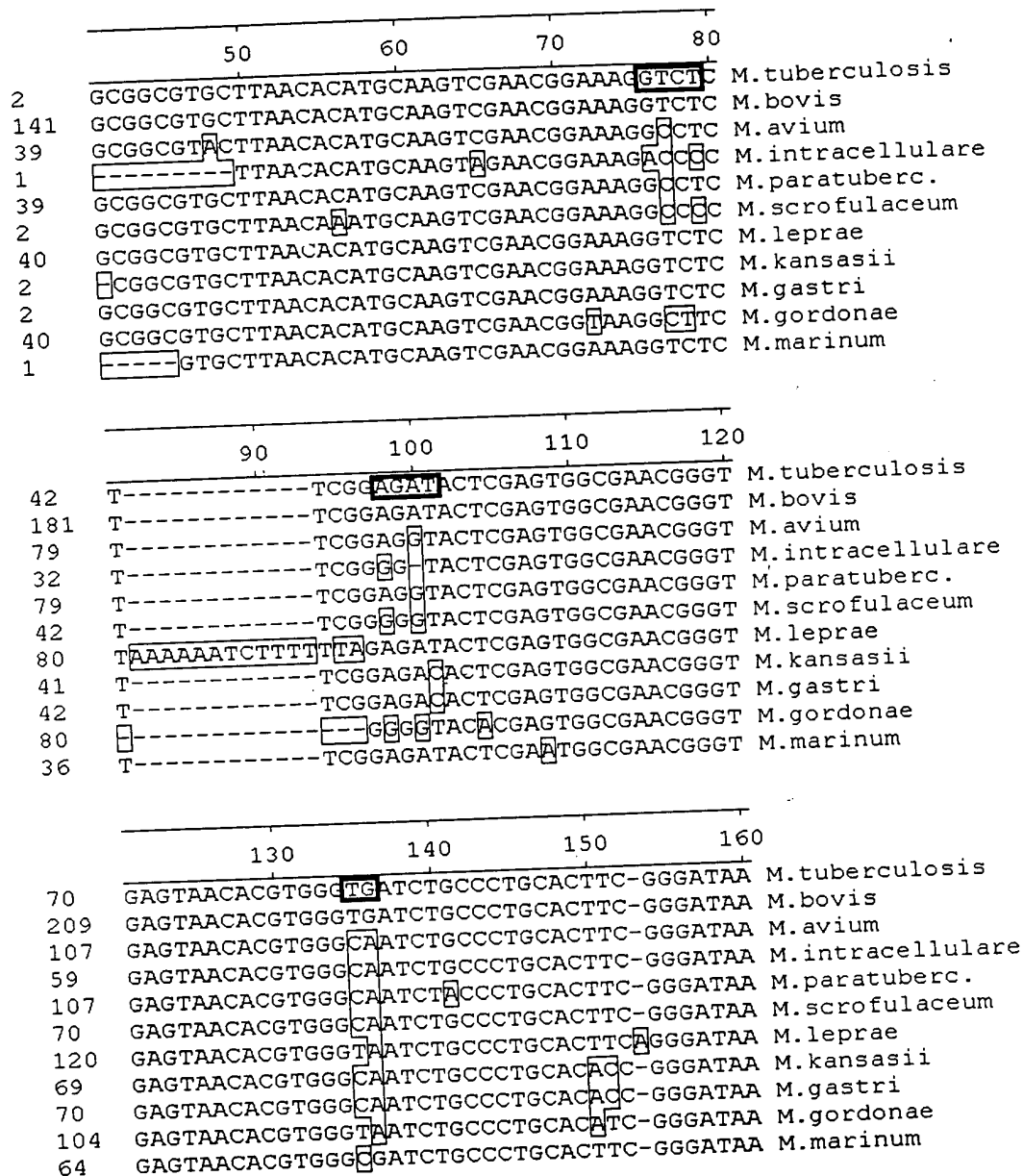


Figure 2A

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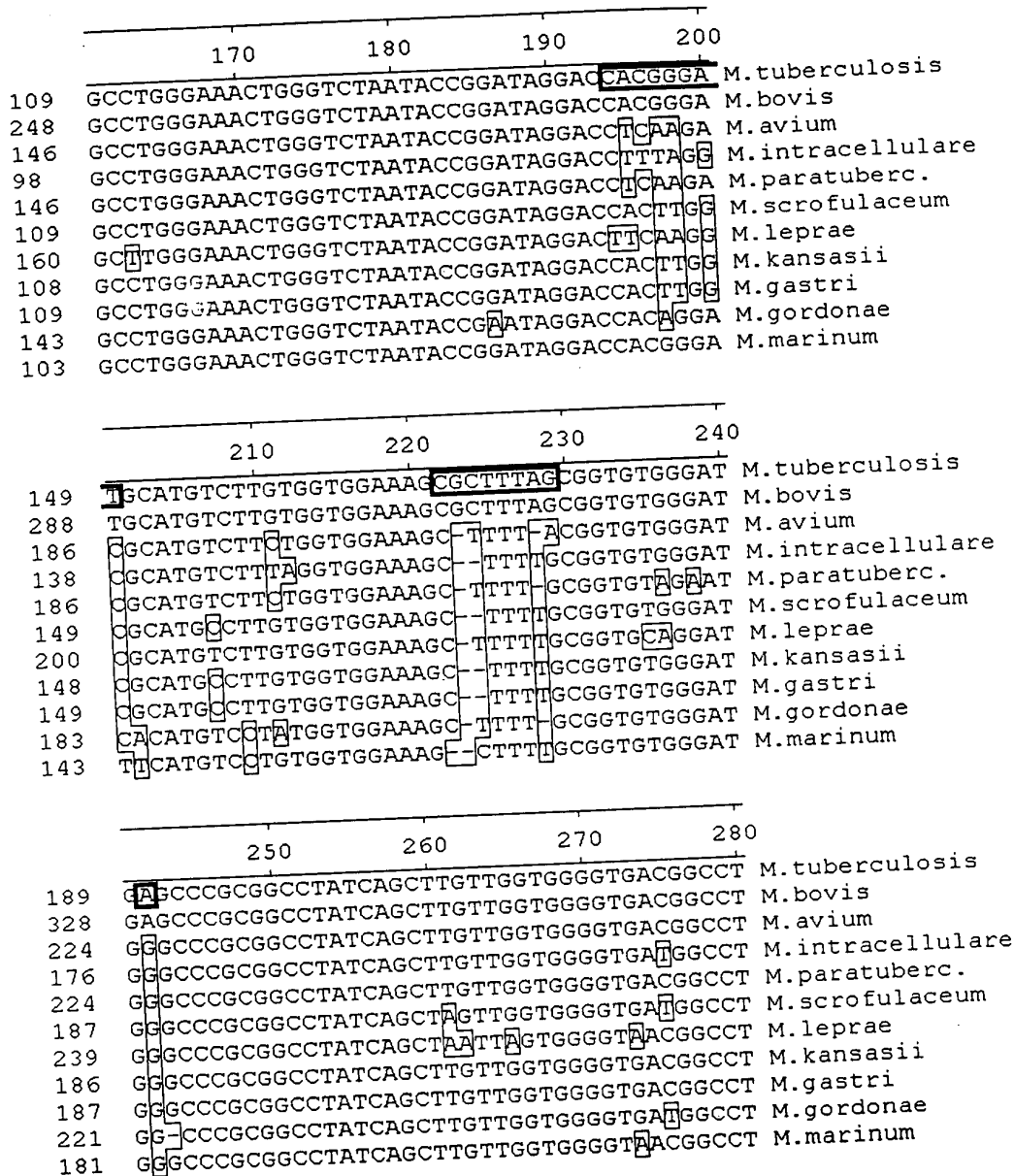


Figure 2B

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	450	460	470	480	
389	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.tuberculosis
528	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.bovis
424	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.avium
376	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.intracellulare
424	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTAGG				M.paratuberc.
387	AAACCTCTTTTACCATCGACGAAGGTCTCA---CTTTGTGG				M.scrofulaceum
439	AAACCTCTTTTACCATCGACGAAGGTCTGGGAATTCTCTCGG				M.leprae
386	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.kansasii
387	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.gastri
420	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.gordonae
381	AAACCTCTTTTACCATCGACGAAGGTCTGGGTTCTCTCGG				M.marinum

	1130	1140	1150	1160	
1069	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.tuberculosis
1208	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.bovis
1104	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.avium
1056	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.intracellulare
1098	TCTCATGTTGCCAGCGGGTAATGCAGGGGACTCGTGAGAG				M.paratuberc.
1064	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.scrofulaceum
1119	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.leprae
1066	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.kansasii
1067	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gastri
1100	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gordonae
1061	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.marinum

	1250	1260	1270	1280	
1189	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.tuberculosis
1328	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.bovis
1224	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.avium
1176	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.intracellulare
1218	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.paratuberc.
1184	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.scrofulaceum
1239	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.leprae
1186	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.kansasii
1187	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.gastri
1220	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.gordonae
1181	CAATGGCCGGTACAAAGGGCTGCGATGCCGAGGTTAAG				M.marinum

Figure 2C

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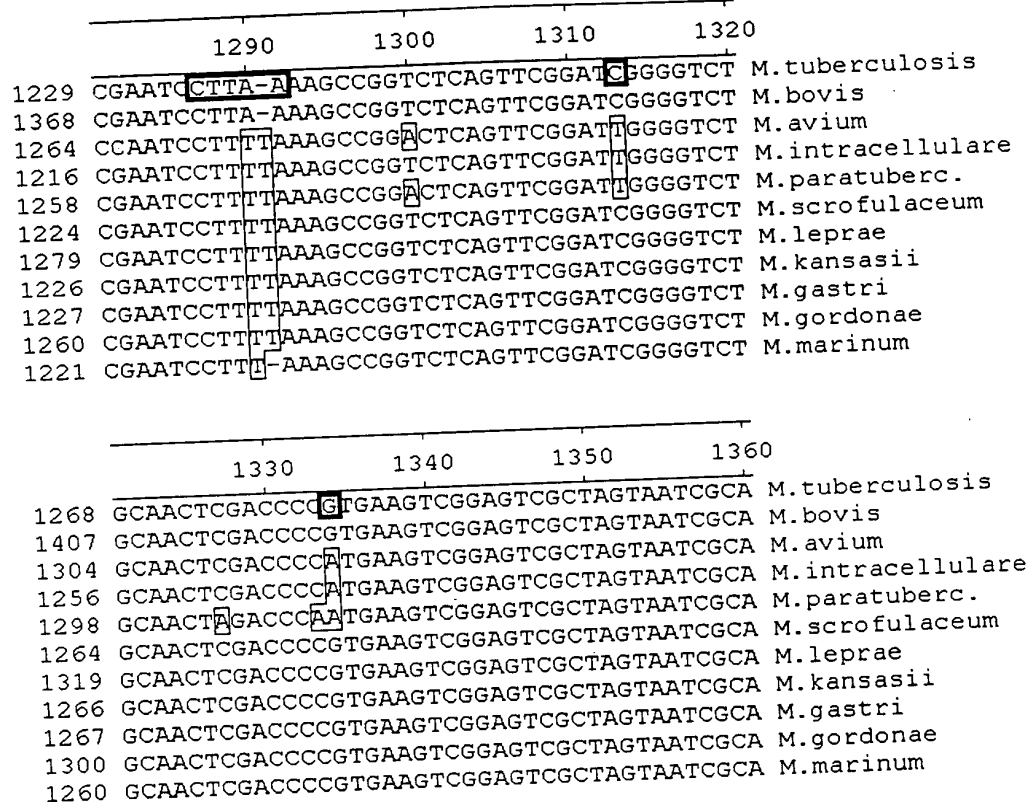


Figure 2D

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		50	60	70	80	
128	TTCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.tuberculosis
39	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC					M.bovis
41	TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCATGATAC					M.phlei
3559	TACCGAACCCGGAAGCTAAGCCTGTCAGCGCCGATGATAC					M.leprae
5743	TCCCGAACCCGGAAGCTAAGCCTGCCAGCCCGATGATAC					M.smegmatis

		90	100	110	120	
168	TGCCCTCTCCGCGG-----TGGAAAAGTAGGACACCGCCGAAC					M.tuberculosis
79	TGCCCCCTCCGGGG-----TGGAAAAGTAGGACACCGCCGAAC					M.bovis
81	TGCCCTCACCCTGGG-----TGGAAAAGTAGGACACCGCCGAAC					M.phlei
3599	TGCCCATTCGGG-----TGGAAAAGTAGGACACCGCCGAAC					M.leprae
5782	TACCCCTTCGGG-----TGGAAAAGTAGGACACCGCCGAAC					M.smegmatis

Figure 3

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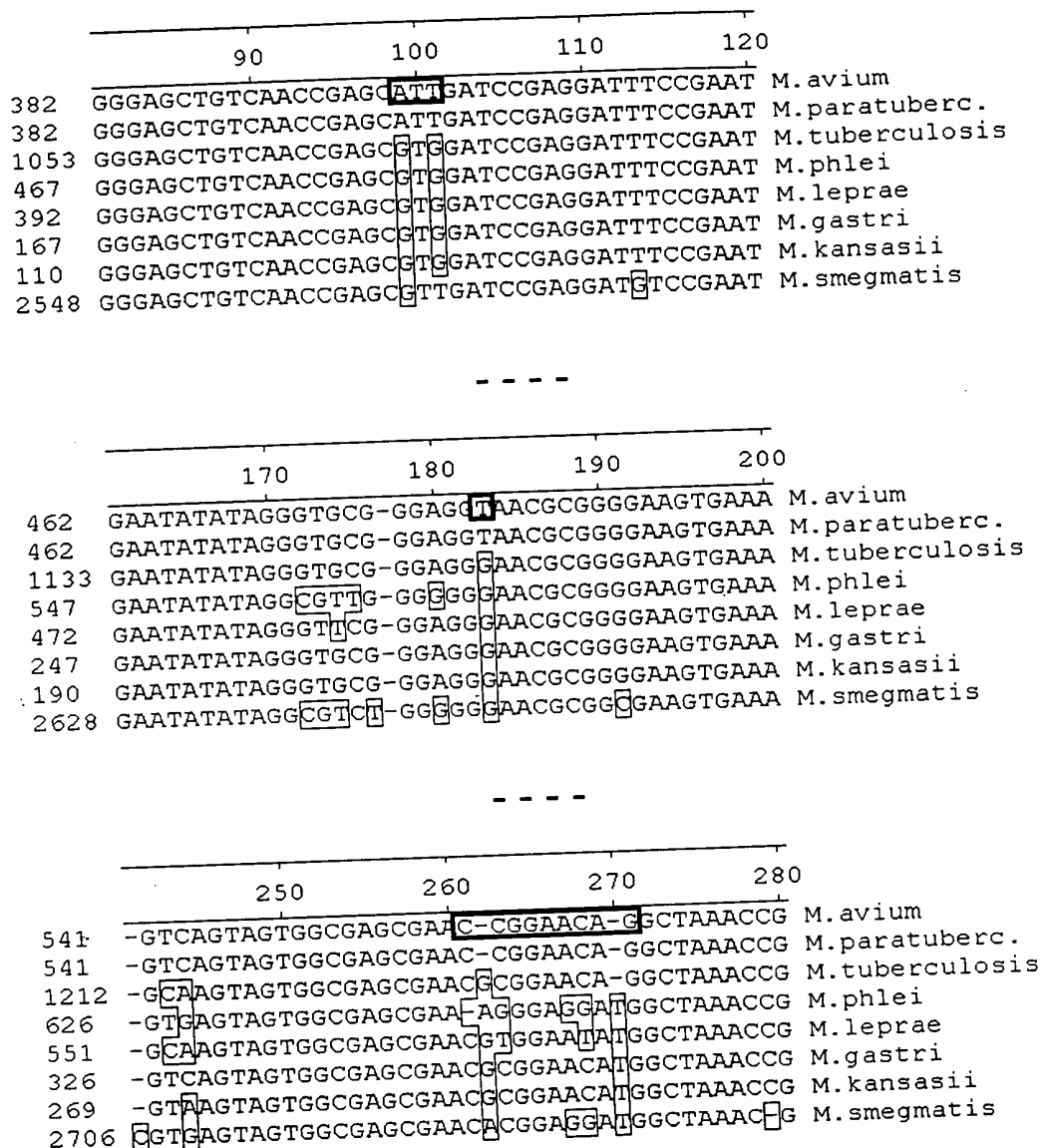


Figure 4A

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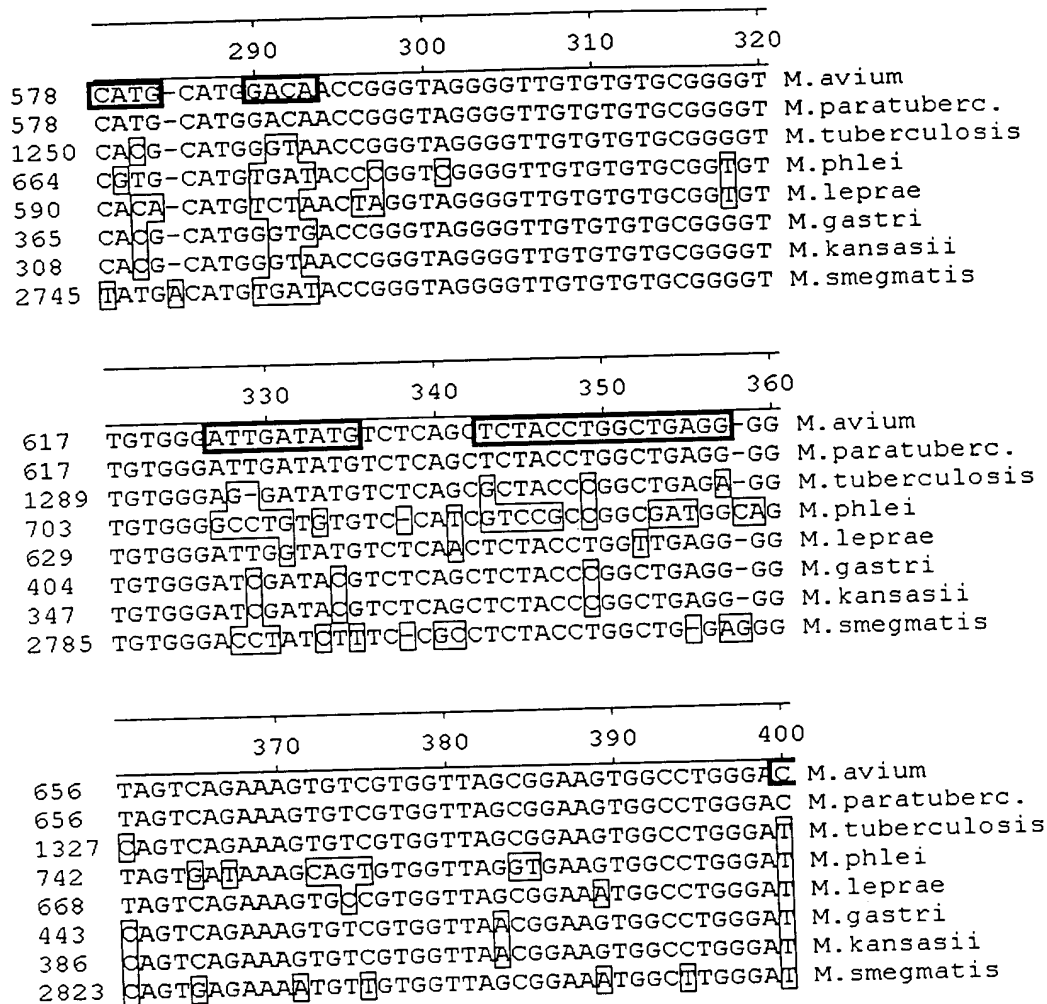


Figure 4B

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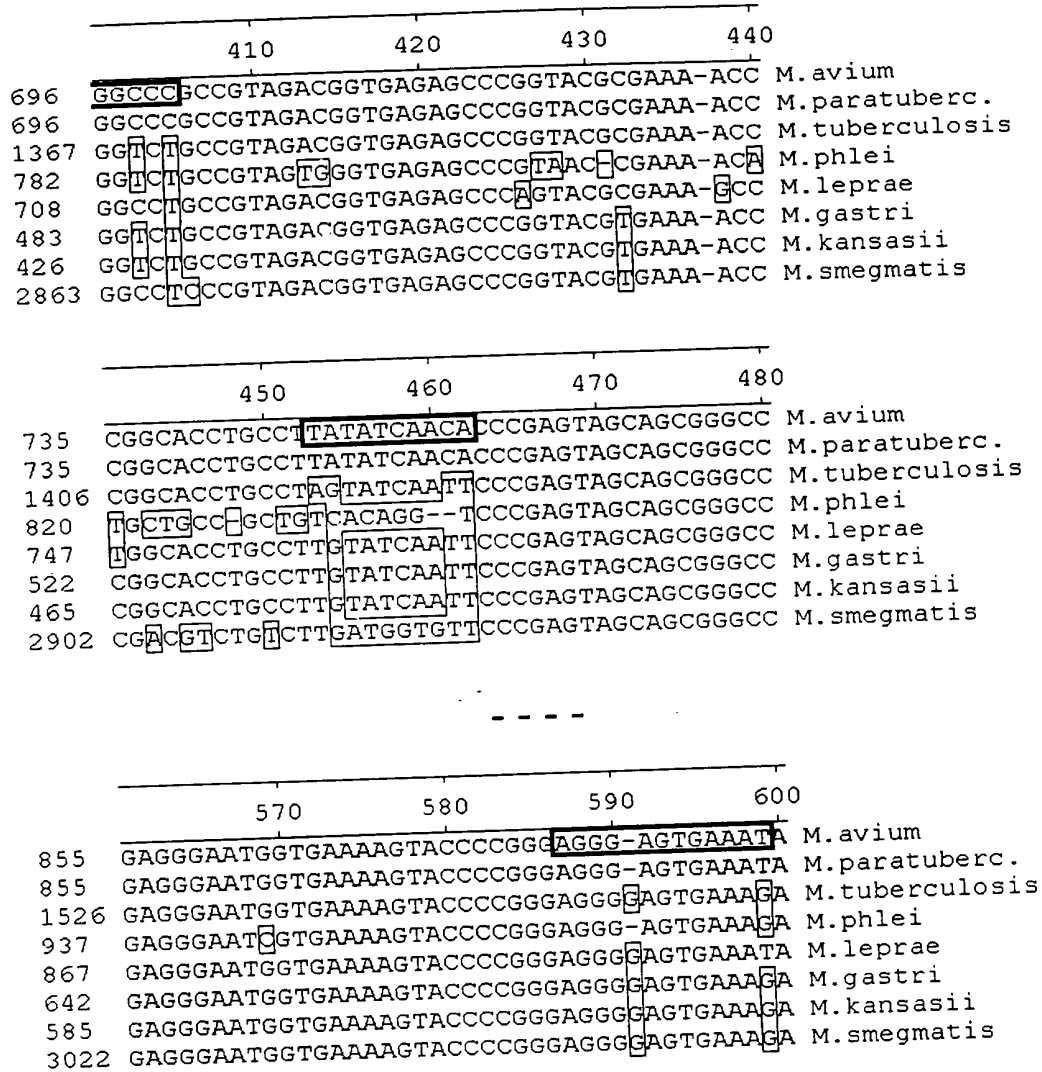


Figure 4C

19/31

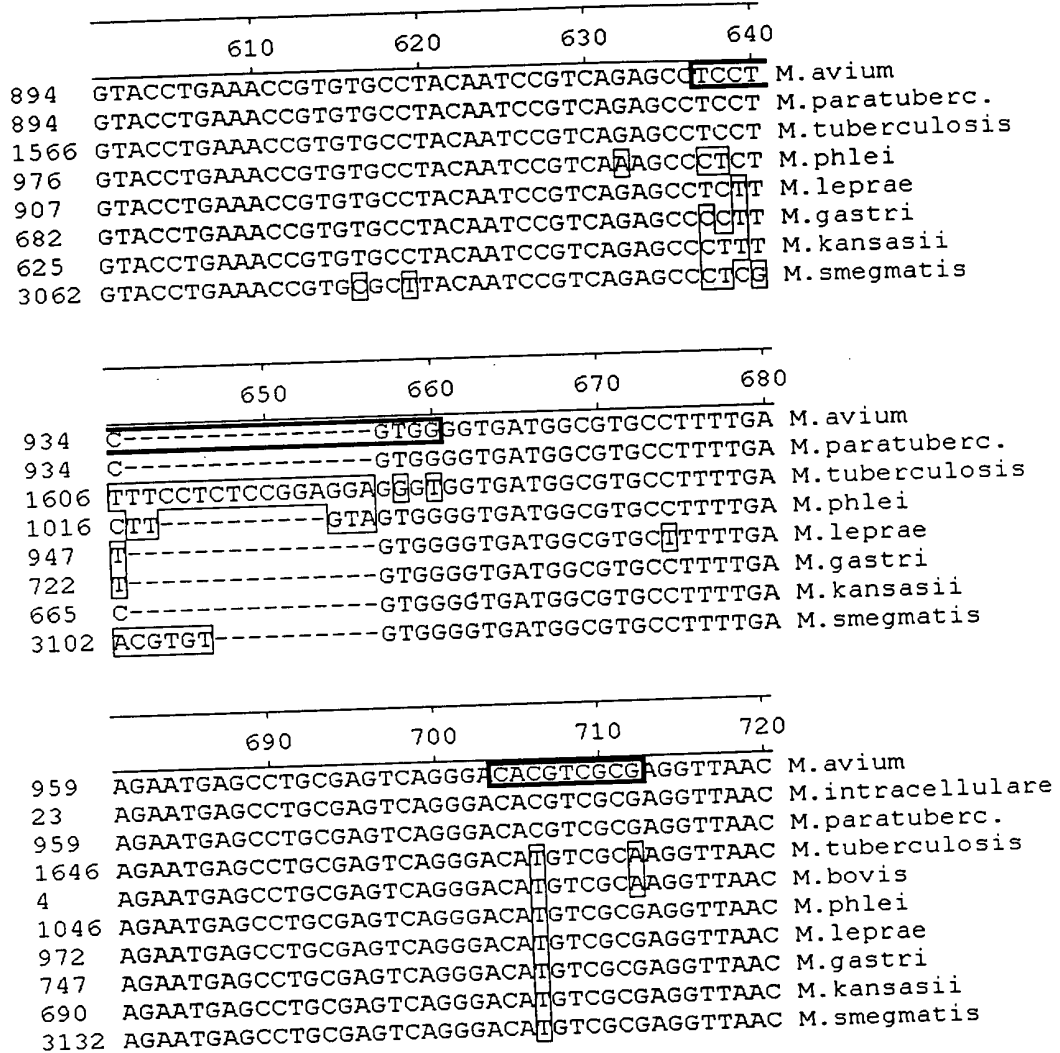


Figure 4D

20/31

770 780 790 800

1039 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.avium
 103 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.intracellulare
 1039 CGCATCCCCTTTGGG-----GTGTAGTGGCGTGT M.paratuberc.
 1726 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M.tuberculosis
 84 CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT M.bovis
 1126 CGTATCCCAACCTGTT-----EGGGTTGTGTAGTGGCGTGT M.phlei
 1052 CGTATCACGTTGTGAGCGT-----GTGTAGTGGCGTGT M.leprae
 827 CGTATCACGCGTAAGCGT-----GTGTAGTGGCGTGT M.gastri
 770 CGTATCGCGCGCGAGCGT-----GTGTAGTGGCGTGT M.kansasii
 3212 CGTATCCACACAAGAGTGTGTG-----GTGTAGTGGCGTGT M.smegmatis

1050 1060 1070 1080

1307 CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA M.avium
 1307 CAGCCAAACTCCGAATGCCG-TGGTG-TAAAAGCGTGGCA M.paratuberc.
 2005 CAGCCAAACTCCGAATGCCG-TGGTG-TAAGCGTGGCA M.tuberculosis
 1401 CAGCCAAACTCCGAATGCCG-TAAG-TAAAAGTGTGGCA M.phlei
 1323 CAGCCAAACTCCGAATGCCG-TGGTT-TAAAAGCGTGGCA M.leprae
 1098 CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA M.gastri
 1041 CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA M.kansasii
 3486 CAGCCAAACTCCGAATGCCG-TAAGGCAAGAGTGGGAA M.smegmatis

1170 1180 1190 1200

1425 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.avium
 1425 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.paratuberc.
 2122 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.tuberculosis
 1519 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.phlei
 1441 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.leprae
 1215 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.gastri
 1158 AGTGGAAAAGGATGTGTAGTCGCAGAGACAAACCAGGAGG M.kansasii
 3606 AGTGGAAAAGGATGTGTAGTCGCAGAGAGAAACCAGGAGG M.smegmatis

Figure 4E

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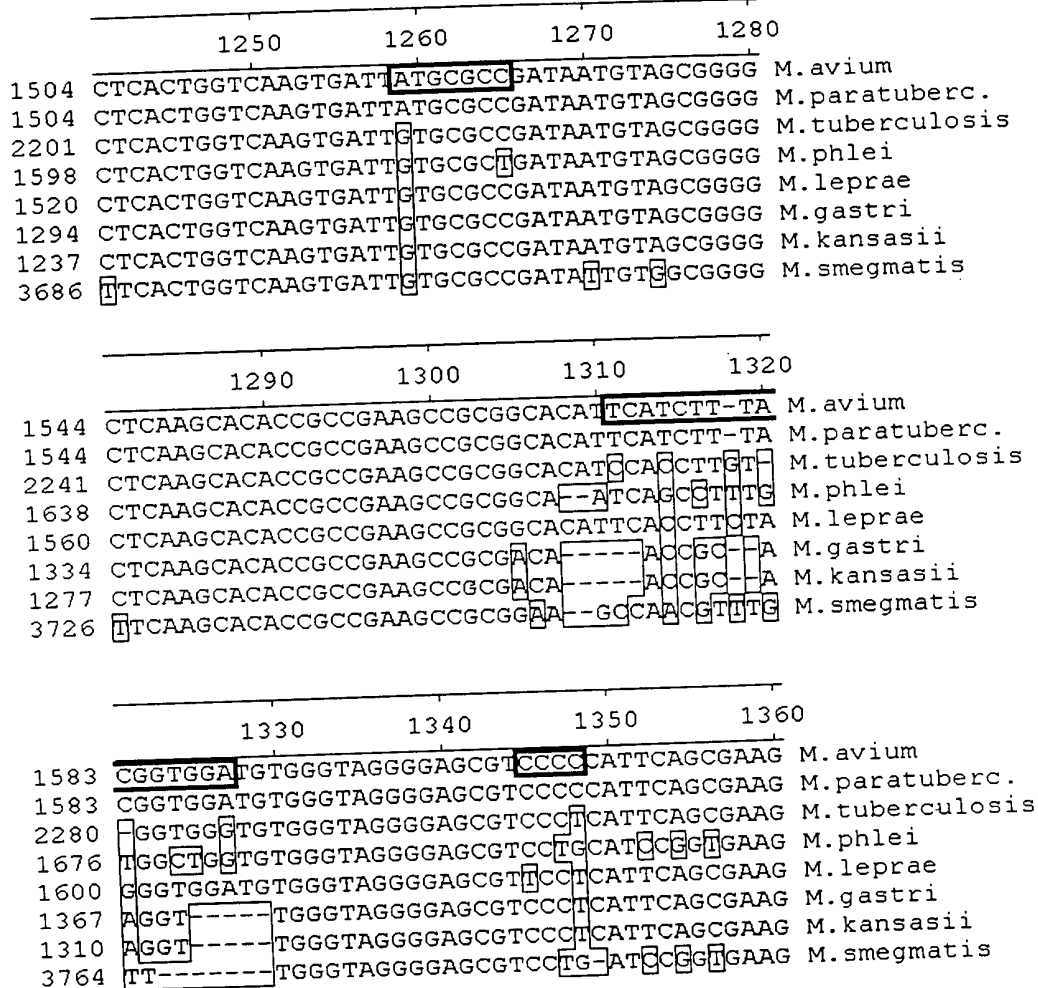


Figure 4F

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1370 1380 1390 1400

1623 CT-CCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.avium
 1623 CT-CCGGGTGA[□]CCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.paratuberc.
 2319 CCACCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT M.tuberculosis
 1716 CCGCCG[□]AGTGA[□]CCGGTGGTGGAGGGTGGGGAGTGAGAAT M.phlei
 1640 CCTCCGGGT[□]AACCGGTGGTGGAGGGTGGGGAGTGAGAAT M.leprae
 1402 CCGCCGGGTGACCGGTGGTGGAGG[□]TGGGGAGTGAGAAT M.gastri
 1345 CTG[□]CCCGGTGACCGGTGGTGGAGG[□]TGGGGAGTGAGAAT M.kansasii
 3796 CCGCCG[□]AGTAT[□]CG[□]AGTGGTGGAGGGT[□]TGGGAGTGAGAAT M.smegmatis

- - - -

1530 1540 1550 1560

1781 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG M.avium
 1781 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATGGG M.paratuberc.
 2479 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGGG M.tuberculosis
 1875 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG[□]AG M.phlei
 1800 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGG[□] M.leprae
 1562 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGGG M.gastri
 1505 CGATGGACAACGGGTTGATATTCCCGTACCCGTGT[□]TGGG M.kansasii
 3956 CGATGGACAACGGGTTGATATTCCCGTACCCGTGTATG[□]G M.smegmatis

1570 1580 1590 1600

1821 CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.avium
 1821 CGTCCCTGATGAATCA-GCGGTACTAACCACCCAAAACCG M.paratuberc.
 2519 CG[□]CC[□]GTGA[□]GAATCA-GCGGTACTAACCACCCAAAACCG M.tuberculosis
 1915 CGTCCCTGATGAATCA[□]TCATT[□]T[□]GCTAACCACCCAAAACCG[□] M.phlei
 1840 CG[□]CC[□]GTGAATCA-GCGGTACT[□]AACCACCCAAAACCG M.leprae
 1602 CG[□]CC[□]GTGAATCA-GCGGTACTAACCACCCAAAACCG M.gastri
 1545 CG[□]CC[□]GTGAATCA-GCGGTACTAACCACCCAAAACCG M.kansasii
 3996 CGTCC[□]ATGAATCA-GCGGTACTAACC[□]CCAAAACCG[□] M.smegmatis

Figure 4G

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	1610	1620	1630	1640	
1860	GAT-CGACCAT-TCCCCTTCGGGGG	C-GTGGCGATT-CGG			M. avium
1860	GAT-CGACCAT-TCCCCTTCGGGGG	C-GTGGCGATT-CGG			M. paratuberc.
2558	GAT-CGATCA-TCCCCTTCGGGGG	TGTGGAGTTT-TGG			M. tuberculosis
1955	GAC-CGATC-ATCC-TTCGGGG	-GTGACGGTTG-GG			M. phlei
1879	GAT-CGACCATATCCCCTTCGGGGG	CTATGGAGGTT-CGG			M. leprae
1641	GAT-CGATCAC-TCCCCTTCGGGGG	A-GTGGAGGTC-TGG			M. gastri
1584	GAT-CGATCAC-TCCCCTTCGGGGG	C-GTGGAGGTC-TGG			M. kansasii
4035	ACCGTGACCGCACCT-TTCGGGG	-TGTGGCGTTGGTGG			M. smegmatis

	1650	1660	1670	1680	
1896	GGCTGCGTGGGACCTTCGCTGGT	AGTAGTAGTCAAGCAATGGG			M. avium
1896	GGCTGCGTGGGACCTTCGCTGGT	AGTAGTAGTCAAGCAATGGG			M. paratuberc.
2594	GGCTGCGTGGGACTTCGCTGGT	AGTAGTAGTCAAGCGATGGG			M. tuberculosis
1986	GGCTGCGTGGGACCG-GTGGGT	AGTAGTAGTCAAGCGATGGG			M. phlei
1917	GGCTGCGTGGGACTTCGTTGGT	AGTAGTAGTCAAGCGATGGG			M. leprae
1677	GGCTGCGTGGGACCTTCGCTGGT	AGTAGTAGTCAAGCGATGGG			M. gastri
1620	GGCTGCGTGGGACCTTCGCTGGT	AGTAGTAGTCAAGCGATGGG			M. kansasii
4071	GGCTGCA-TGGGACCTTCGTTGGT	AGTAGTAGTCAAGCGATGGG			M. smegmatis

	1690	1700	1710	1720	
1936	-GTGACGCAGGAAGGCAGCCGT	ACCAGTCAGTGGTAATA-			M. avium
1936	-GTGACGCAGGAAGGCAGCCGT	ACCAGTCAGTGGTAATA-			M. paratuberc.
2634	-GTGACGCAGGAAGGTAGCCGT	ACCAGTCAGTGGTAATA-			M. tuberculosis
2025	-GTGACGCAGGAAGGTAGCCGT	ACCAGTCAGTGGTAATA-			M. phlei
1957	-GTGACGCAGGAAGGTAGCCGT	ACCAGTCAGTGGTAATA-			M. leprae
1717	-GTGACGCAGGAAGGCAGCCGT	ACCAGTCAGTGGTAATA-			M. gastri
1660	-GTGACGCAGGAAGGCAGCCGT	ACCAGTCAGTGGTAATA-			M. kansasii
4111	-GTGACGCAGGAAGGTAGCCGT	ACCAGTCAGTGGTAATA-			M. smegmatis

	1730	1740	1750	1760	
1974	-CTGGGGCAAGCCCGTAG--AG	AGCGATAGGCAAATCCGT			M. avium
1974	-CTGGGGCAAGCCCGTAG--AG	AGCGATAGGCAAATCCGT			M. paratuberc.
2672	-CTGGGGCAAGCCCGTAGGGAG	AGCGATAGGCAAATCCGT			M. tuberculosis
2063	-CTGGGGCAAGCCCGTAGGGAG	AGCGATAGGCAAATCCGT			M. phlei
1995	-CTGGGGCAAGCCCGTAGGGAG	AGCGATAGGCAAATCCGT			M. leprae
1755	-CTGGGGCAAGCCCGTAGGGAG	AGCGATAGGCAAATCCGT			M. gastri
1698	-CTGGGGCAAGCCCGTAGGGAG	AGCGATAGGCAAATCCGT			M. kansasii
4149	-CTGGGGCAAGCCCGTAGGGAG	TCAGATAGGCAAATCCGT			M. smegmatis

Figure 4H

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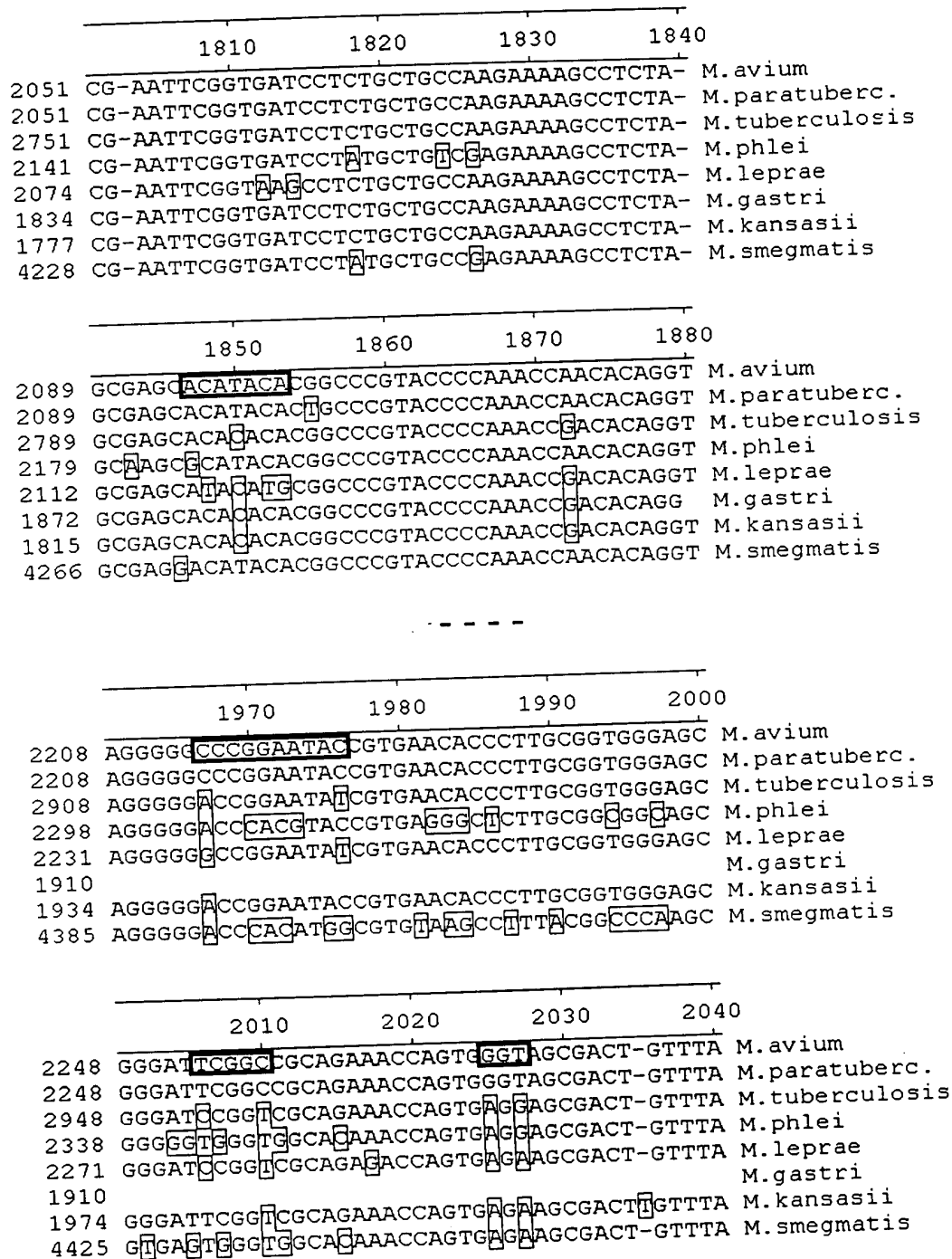


Figure 4I

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	2130	2140	2150	2160	
2367	CCGTTAACCC	GT	--AAGGGTGAAGCGGAGAATTTAAGCCC		M.avium
2367	CCGTTAACCCGT	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.paratuberc.
3067	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.tuberculosis
2457	CCGTTAACCC	TTTCGGGGGTGAAGCGGAGAATTTAAGCCC			M.phlei
2390	CTGTTAACCCGA	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.leprae
1910					M.gastri
2094	CCGTTAACCCG	--AAGGGTGAAGCGGAGAATTTAAGCCC			M.kansasii
4544	CCGTTAACCC	CCTTGGGGGTGAAGCGGAGAATTTAAGCCC			M.smegmatis

	2250	2260	2270	2280	
2485	GTAACGACTTC	CCAA	CTGTCTCAACCATAGACTCGGCGAA		M.avium
2485	GTAACGACTTCCCAACTGTCTCAACCATAGACTCGGCGAA				M.paratuberc.
3185	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.tuberculosis
2577	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.phlei
2508	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.leprae
1910					M.gastri
2212	GTAACGACTTCTCAACTGTCTCAACCATAGACTCGGCGAA				M.kansasii
4663	GTAACGACTTCTCAACTGTCTCAAC	ATAGACTCGGCGAA			M.smegmatis

	2370	2380	2390	2400	
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.avium
2605	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTTTGAA				M.paratuberc.
3305	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.tuberculosis
2697	GTCGATACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.phlei
2628	GTTTCGGTTCGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.leprae
1910					M.gastri
2332	GTTTCGGTACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.kansasii
4782	GTCGATACGGTTTGTGTAGGATAGGTGGGAGACTGTGAA				M.smegmatis

Figure 4J

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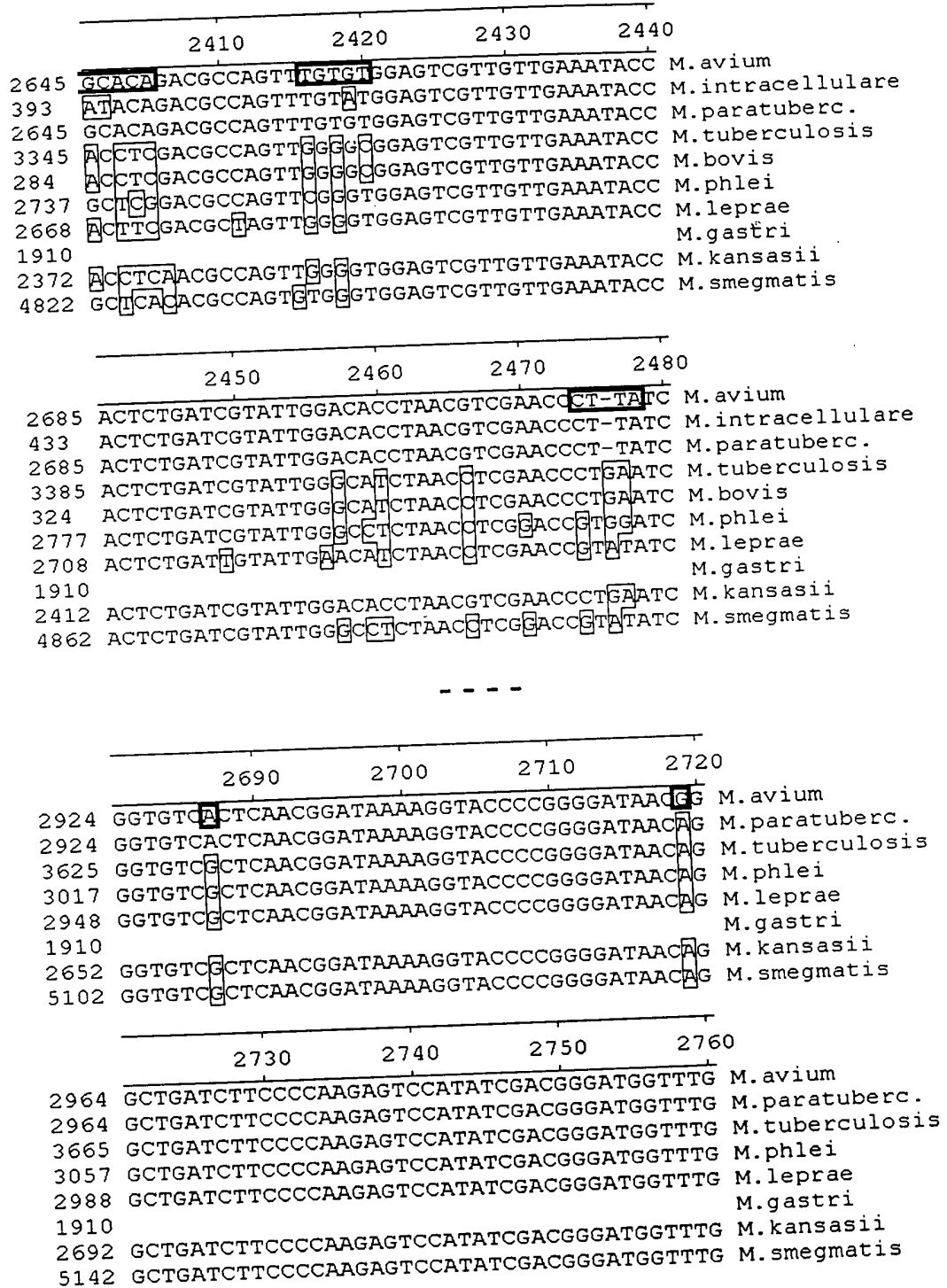


Figure 4K

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	2770	2780	2790	2800	
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. avium
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. paratuberc.
3705	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. tuberculosis
3097	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. phlei
3028	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. leprae
1910					M. gastri
2732	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. kansasii
5182	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. smegmatis
	2810	2820	2830	2840	
3044	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. avium
3044	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. paratuberc.
3745	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. tuberculosis
3137	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. phlei
3068	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. leprae
1910					M. gastri
2772	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. kansasii
5222	GGTCCCAAGGGTTGGGCTGTTGCGCC-ATTAAAGCGGCAC				M. smegmatis

	3050	3060	3070	3080	
3283	CAAGATCAGGTTT-CTCACCC	TTTTAGAGGGATAAGGCC			M. avium
638	CAAGATCAGGTTT-CTCACCC	TTTTAGAGGGATAAGGCC			M. intracellulare
3283	CAAGATCAGGTTT-CTCACCC	TTTTAGAGGGATAAGGCC			M. paratuberc.
3984	CAAGATCAGGTTT-CTCACCC	ACTTGGTGGGATAAGGCC			M. tuberculosis
570	CAAGATCAGGTTT-CTCACCC	ACTTGGTGGGATAAGGCC			M. bovis
3376	CAAGATCAGGTTT-CTCACCC	CTAGGAGGGATAAGGCC			M. phlei
3307	CAA				M. leprae
1910					M. gastri
3011	CAAGATCAGGTTT-CTCACCC	ACTTGGTGGGATAAGGCC			M. kansasii
5462	CAAGATCAGGTTT-CTCACCC	CTAGGAGGGATAAGGCC			M. smegmatis
	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. avium
677	CCCGC-AGACCACGGG	TTGATAGGCC	CAGACCTGGAAGCT		M. intracellulare
3322	CCCGC-AGATCACGGG	ATTGATAGGCC	CAGACCTGGAAGCT		M. paratuberc.
4023	CCCGC-AGAACACGGG	TTCAATAGGT	CAGACCTGGAAGCT		M. tuberculosis
609	CCCGC-AGAACACGGG	TTCAATAGGT	CAGACCTGGAAGCT		M. bovis
3415	CCCGC-AGACCACGGG	ATGATAGGC	CAGACCTGGAAGCT		M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGAACACGGG	TTGATAGGCC	CAGACCTGGAAGCT		M. kansasii
5501	CCCGC-AGACCACGGG	ATTGATAGGC	CAGACCTGGAAGCT		M. smegmatis

Figure 4L

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		130	140	150	160	
107	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.avium
59	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.intracellulare
107	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.paratuberc.
70	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.scrofulaceum
70	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.tuberculosis
209	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.bovis
120	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.leprae
69	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.kansasii
70	GAGTAACACGTGGGCAATCTGCCCTGCACTTC	-GGGATAA				M.gastri
104	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.gordonae
64	GAGTAACACGTGGG	CA	ATCTGCCCTGCACTTC	-GGGATAA		M.marinum

- - - -

		450	460	470	480	
424	AAACCTCTTTCACCATCGACGAAGGTCCGGG	TTTT	CTCGG			M.avium
376	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTTTCTCGG					M.intracellulare
424	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTTTCTAGG					M.paratuberc.
387	AAACCTCTTTCACCATCGACGAAGGTCTCA	---CTTCTGG				M.scrofulaceum
389	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.tuberculosis
528	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.bovis
439	AAACCTCTTTCACCATCGACGAAGGTCTGGG	ATTCTCGG				M.leprae
386	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.kansasii
387	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTCTCTCGG					M.gastri
420	AAACCTCTTTCACCATCGACGAAGGTCCGGGTTTTCTCGG					M.gordonae
381	AAACCTCTTTCACCATCGACGAAGGTCTCGG	TTTTCTCGG				M.marinum

		490	500	510	520	
429	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.tuberculosis
568	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.bovis
464	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.avium
416	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.intracellulare
464	ATTGACGGTAGGTGGAGAAGAAGCAC	-----	ACTACGTG			M.paratuberc.
424	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.scrofulaceum
479	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.leprae
426	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.kansasii
427	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.gastri
460	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.gordonae
421	ATTGACGGTAGGTGGAGAAGAAGCACCGGCCAACTACGTG					M.marinum

Figure 5A

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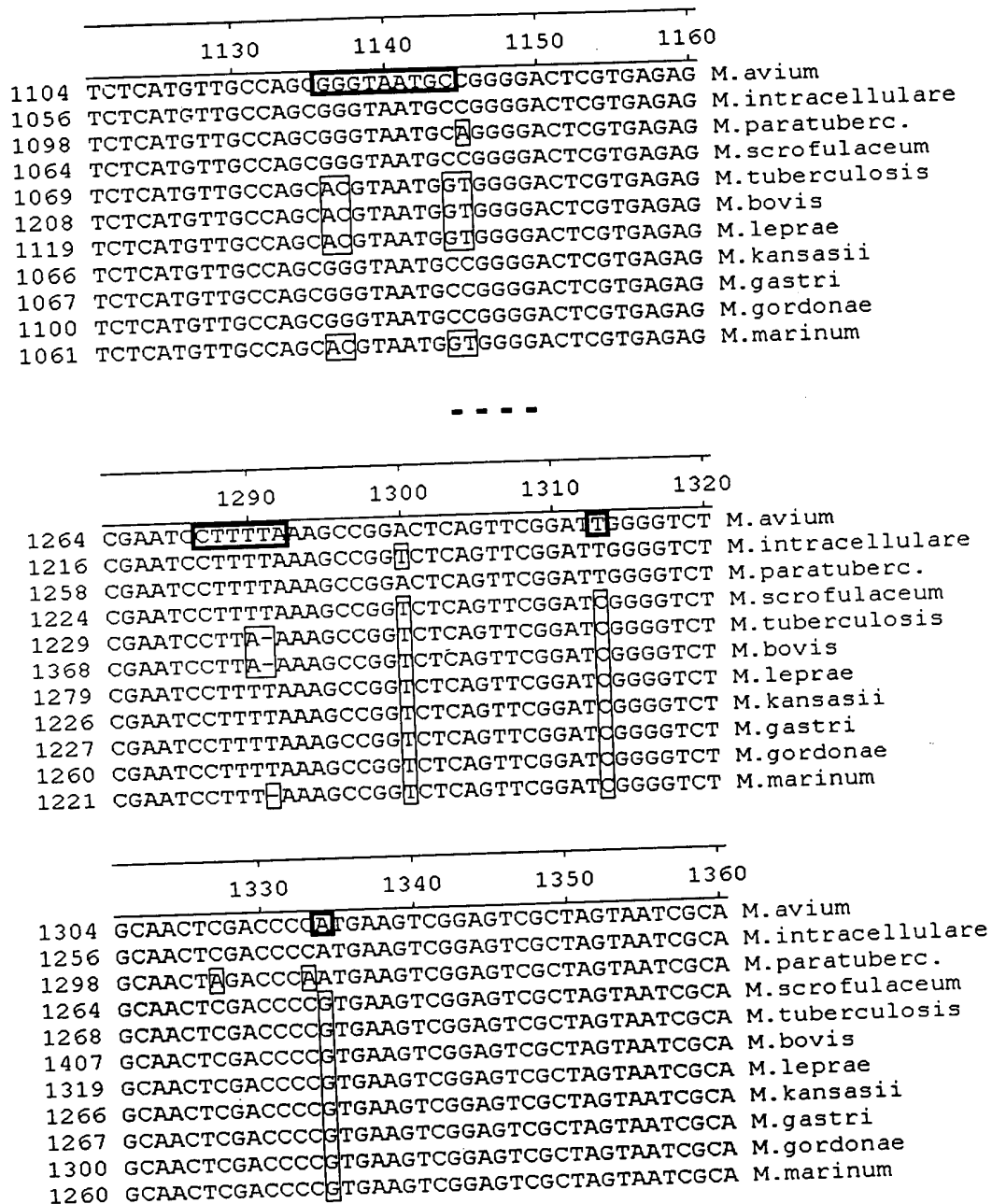


Figure 5B

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2550 | TTACGGCGGCAGGACGAAAGACCCCGGGACCTTCACTA 2589 |
2568 2569 |

Mavirus 23S:

Figure 6

441 | TGGAGAGAGAGCACCAGGCGCCAACTACGTGCCAGCAGCCGGGTAATACGTAG 491
473 474 477 |
452 |
843 | GTACGCGCGCAGGCTAAACTCAAGGAATTGACGGGGGC 883
863 866 |

M. tuberculosis 16S:

Figure 7